

c1 in SEQ ID NO:5 and the dapA promotor comprising the MA20 mutation as set forth in SEQ ID NO:6 and whereby said overexpression of said wild type pyc gene of Corynebacterium glutamicum or said wild type dapA gene of Corynebacterium glutamicum gives a pyruvate carboxylase activity or dihydrodipicolinate synthase activity above the level of a wild type Corynebacterium glutamicum.

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c2 3. (Twice Amended) Bacteria of claim 1, in which a lysE gene of Corynebacterium glutamicum encoding the lysine export carrier is overexpressed, wherein overexpression of said LysE gene is achieved by increasing the copy number of LysE genes.

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c3 22. (Twice Amended) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 5.

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23. (Twice Amended) An isolated DNA comprising the nucleotide sequence shown in SEQ ID NO: 6.

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28. (Amended) Bacteria of claim 27, wherein said aspartate kinase is resistant to inhibition and/or threonine.

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c4 29. (Amended) Bacteria of claim 1, wherein said dapA gene including a dapA promotor selected from the group consisting of: the dapA promotor comprising the MC20 mutation as set forth in SEQ ID NO:5 and the dapA promotor comprising the MA20 mutation as set forth in SEQ ID NO:6 wherein said dapA gene, including said dapA promoter is inserted into a aecD (amino ethyl cysteine degrading) gene of Corynebacterium glutamicum.

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30. (Amended) L-Lysine-producing bacteria of the species Corynebacterium glutamicum comprising an overexpressed wild type pyc gene of Corynebacterium glutamicum encoding pyruvate carboxylase, an overexpressed wild type dapA gene of Corynebacterium glutamicum encoding dihydrodipicolinate synthase, and an overexpressed wild type lysE gene of Corynebacterium glutamicum encoding lysine export carrier.

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31. (Amended) Bacteria of claim 30 further comprising an overexpressed lysC gene of Corynebacterium glutamicum encoding aspartate kinase.